



# SEQUENCE LISTING

<110> Dale, James B.

<120> GROUP A STREPTOCOCCAL VACCINES

<130> 481112.410

<140> US 09/151,409

<141> 1998-09-10

<150> US 60/058,635

<151> 1997-09-12

<160> 16

<170> PatentIn Ver. 2.0

<210> 1

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Product of  
Synthesis -- Primer, hybridizes to streptococcal  
type 24 M protein DNA

<400> 1

ggggggggcat cggtcgcgac taggtctcag acagat

36

<210> 2

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Product of  
Synthesis -- Primer, hybridizes to streptococcal  
type 24 M protein DNA

<400> 2

gggggggggat ccacgtagtt tctctttagc

30

<210> 3

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Product of  
Synthesis -- Primer, hybridizes to streptococcal  
type 5 M protein DNA

<400> 3

gggggggggat ccgccgtgac taggggtaca

30

<210> 4  
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<212> DNA  
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<223> Description of Artificial Sequence: Product of  
Synthesis -- Primer, hybridizes to streptococcal  
type 5 M protein DNA

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<400> 4  
gggggggtcg acctcagttt ttaacccttc 30

<210> 5  
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<223> Description of Artificial Sequence: Product of  
Synthesis -- Primer, hybridizes to streptococcal  
type 6 M protein DNA

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gggggggtcg acagagtgtt tcctaggggg 30

<210> 6  
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<212> DNA  
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<223> Description of Artificial Sequence: Product of  
Synthesis -- Primer, hybridizes to streptococcal  
type 6 M protein DNA

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ggggggccat ggtaacttgt cattattagc 30

<210> 7  
<211> 30  
<212> DNA  
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<223> Description of Artificial Sequence: Product of  
Synthesis -- Primer, hybridizes to streptococcal  
type 19 M protein DNA

<400> 7  
ggggggccat ggagagtgcg ttatactagg 30

<210> 8  
<211> 30  
<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Product of  
Synthesis -- Primer, hybridizes to streptococcal  
type 19 M protein DNA

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<400> 8  
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30

<210> 9  
<211> 30  
<212> DNA  
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<223> Description of Artificial Sequence: Product of  
Synthesis -- Primer, hybridizes to streptococcal  
type 1 M protein DNA

<400> 9  
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<210> 10  
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<212> DNA  
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<223> Description of Artificial Sequence: Product of  
Synthesis -- Primer, hybridizes to streptococcal  
type 1 M protein DNA

<400> 10  
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<210> 11  
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<212> DNA  
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<223> Description of Artificial Sequence: Product of  
Synthesis -- Primer, hybridizes to streptococcal  
type 3 M protein DNA

<400> 11  
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<210> 12  
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<212> DNA  
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<223> Description of Artificial Sequence: Product of  
Synthesis -- Primer, hybridizes to streptococcal  
type 3 M protein DNA

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gggggggatcg atatttaact cttgtaacag

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<210> 13  
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<212> DNA  
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<223> Description of Artificial Sequence: Product of  
Synthesis -- Primer, hybridizes to streptococcal  
type 24 M protein DNA

<400> 13  
gggggggatcg atgtcgcgac taggtctcag

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<210> 14  
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Product of  
Synthesis -- Primer, hybridizes to streptococcal  
type 24 M protein DNA

<400> 14  
ggggggaagc ttttacttac gtgcctctaa ttc

33

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<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Hexavalent M  
fusion gene sequence constructed from  
streptococcal type 24, 5, 6, 19, 1 and 3 M protein  
DNAs

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<222> (1)..(1149)

<400> 15  
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Ala Cys Met Val Ala Thr Arg Ser Gln Thr Asp Thr Leu Glu Lys Val

48

1	5	10	15	
caa gaa cgt gct gac aag ttt gag ata gaa aac aat acg tta aaa ctt				96
Gln Glu Arg Ala Asp Lys Phe Glu Ile Glu Asn Asn Thr Leu Lys Leu				
20		25	30	
aag aat agt gac tta agt ttt aat aat aaa gcg tta aaa gat cat aat				144
Lys Asn Ser Asp Leu Ser Phe Asn Asn Lys Ala Leu Lys Asp His Asn				
35	40	45		
gat gag tta act gaa gag ttg agt aat gct aaa gag aaa cta cgt gga				192
Asp Glu Leu Thr Glu Glu Leu Ser Asn Ala Lys Glu Lys Leu Arg Gly				
50	55	60		
tcc gcc gtg act agg ggt aca ata aat gac ccg caa aga gca aaa gaa				240
Ser Ala Val Thr Arg Gly Thr Ile Asn Asp Pro Gln Arg Ala Lys Glu				
65	70	75	80	
gct ctt gac aag tat gag cta gaa aac cat gac tta aaa act aag aat				288
Ala Leu Asp Lys Tyr Glu Leu Glu Asn His Asp Leu Lys Thr Lys Asn				
85	90	95		
gaa ggg tta aaa act gag aat gaa ggg tta aaa act gag aat gaa ggg				336
Glu Gly Leu Lys Thr Glu Asn Glu Gly Leu Lys Thr Glu Asn Glu Gly				
100	105	110		
tta aaa act gag aat gaa ggg tta aaa act gag gtc gac aga gtg ttt				384
Leu Lys Thr Glu Asn Glu Gly Leu Lys Thr Glu Val Asp Arg Val Phe				
115	120	125		
cct agg ggg acg gta gaa aac ccg gac aaa gca cga gaa ctt ctt aac				432
Pro Arg Gly Thr Val Glu Asn Pro Asp Lys Ala Arg Glu Leu Leu Asn				
130	135	140		
aag tat gac gta gag aac tct atg tta caa gct aat aat gac aag tta				480
Lys Tyr Asp Val Glu Asn Ser Met Leu Gln Ala Asn Asn Asp Lys Leu				
145	150	155	160	
cca tgg aga gtg cgt tat act agg cat acg cca gaa gat aag cta aaa				528
Pro Trp Arg Val Arg Tyr Thr Arg His Thr Pro Glu Asp Lys Leu Lys				
165	170	175		
aaa att att gac gat ctt gac gca aaa gaa cat gaa tta caa caa cag				576
Lys Ile Ile Asp Asp Leu Asp Ala Lys Glu His Glu Leu Gln Gln Gln				
180	185	190		
aat gag aag tta tct ctg cag aac ggt gat ggt aat cct agg gaa gtt				624
Asn Glu Lys Leu Ser Leu Gln Asn Gly Asp Gly Asn Pro Arg Glu Val				
195	200	205		
ata gaa gat ctt gca gca aac aat ccc gca ata caa aat ata cgt tta				672
Ile Glu Asp Leu Ala Ala Asn Asn Pro Ala Ile Gln Asn Ile Arg Leu				
210	215	220		
cgt cac gaa aac aag gac tta aaa gcg aga tta gag aat gca atg gaa				720
Arg His Glu Asn Lys Asp Leu Lys Ala Arg Leu Glu Asn Ala Met Glu				
225	230	235	240	

ggt acc ttg tta gat cag gtt	768
Val Ala Gly Arg Asp Phe Lys Arg Ala Gly Thr Leu Leu Asp Gln Val	
245 250 255	
aca caa tta tat act aaa cat aat agt aat tac caa caa tat aat gca	816
Thr Gln Leu Tyr Thr Lys His Asn Ser Asn Tyr Gln Gln Tyr Asn Ala	
260 265 270	
caa gct ggc aga ctt gac ctg aga caa aag gct gaa tat cta aaa ggc	864
Gln Ala Gly Arg Leu Asp Leu Arg Gln Lys Ala Glu Tyr Leu Lys Gly	
275 280 285	
ctt aat gat tgg gct gag agg ctg tta caa gag tta aat atc gat gtc	912
Leu Asn Asp Trp Ala Glu Arg Leu Leu Gln Glu Leu Asn Ile Asp Val	
290 295 300	
gcg act agg tct cag aca gat act ctg gaa aaa gta caa gaa cgt gct	960
Ala Thr Arg Ser Gln Thr Asp Thr Leu Glu Lys Val Gln Glu Arg Ala	
305 310 315 320	
gac aag ttt gag ata gaa aac aat acg tta aaa ctt aag aat agt gac	1008
Asp Lys Phe Glu Ile Glu Asn Asn Thr Leu Lys Leu Lys Asn Ser Asp	
325 330 335	
tta agt ttt aat aat aaa gcg tta aaa gat cat aat gat gag tta act	1056
Leu Ser Phe Asn Asn Lys Ala Leu Lys Asp His Asn Asp Glu Leu Thr	
340 345 350	
gaa gag ttg agt aat gct aaa gag aaa cta cgt aaa aat gat aaa tca	1104
Glu Glu Leu Ser Asn Ala Lys Glu Lys Leu Arg Lys Asn Asp Lys Ser	
355 360 365	
cta tct gaa aaa gct agt aaa att caa gaa tta gag gca cgt aag	1149
Leu Ser Glu Lys Ala Ser Lys Ile Gln Glu Leu Glu Ala Arg Lys	
370 375 380	
taaaagctt	1158

<210> 16

<211> 383

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hexavalent M  
fusion gene sequence constructed from  
streptococcal type 24, 5, 6, 19, 1 and 3 M protein  
DNAs

<400> 16

Ala Cys Met Val Ala Thr Arg Ser Gln Thr Asp Thr Leu Glu Lys Val
1 5 10 15

Gln Glu Arg Ala Asp Lys Phe Glu Ile Glu Asn Asn Thr Leu Lys Leu
20 25 30

Lys Asn Ser Asp Leu Ser Phe Asn Asn Lys Ala Leu Lys Asp His Asn

35

40

45

Asp Glu Leu Thr Glu Glu Leu Ser Asn Ala Lys Glu Lys Leu Arg Gly  
50 55 60

Ser Ala Val Thr Arg Gly Thr Ile Asn Asp Pro Gln Arg Ala Lys Glu  
65 70 75 80

Ala Leu Asp Lys Tyr Glu Leu Glu Asn His Asp Leu Lys Thr Lys Asn  
85 90 95

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Glu Gly Leu Lys Thr Glu Asn Glu Gly Leu Lys Thr Glu Asn Glu Gly  
100 105 110

Leu Lys Thr Glu Asn Glu Gly Leu Lys Thr Glu Val Asp Arg Val Phe  
115 120 125

Pro Arg Gly Thr Val Glu Asn Pro Asp Lys Ala Arg Glu Leu Leu Asn  
130 135 140

Lys Tyr Asp Val Glu Asn Ser Met Leu Gln Ala Asn Asn Asp Lys Leu  
145 150 155 160

Pro Trp Arg Val Arg Tyr Thr Arg His Thr Pro Glu Asp Lys Leu Lys  
165 170 175

Lys Ile Ile Asp Asp Leu Asp Ala Lys Glu His Glu Leu Gln Gln Gln  
180 185 190

Asn Glu Lys Leu Ser Leu Gln Asn Gly Asp Gly Asn Pro Arg Glu Val  
195 200 205

Ile Glu Asp Leu Ala Ala Asn Asn Pro Ala Ile Gln Asn Ile Arg Leu  
210 215 220

Arg His Glu Asn Lys Asp Leu Lys Ala Arg Leu Glu Asn Ala Met Glu  
225 230 235 240

Val Ala Gly Arg Asp Phe Lys Arg Ala Gly Thr Leu Leu Asp Gln Val  
245 250 255

Thr Gln Leu Tyr Thr Lys His Asn Ser Asn Tyr Gln Gln Tyr Asn Ala  
260 265 270

Gln Ala Gly Arg Leu Asp Leu Arg Gln Lys Ala Glu Tyr Leu Lys Gly  
275 280 285

Leu Asn Asp Trp Ala Glu Arg Leu Leu Gln Glu Leu Asn Ile Asp Val  
290 295 300

Ala Thr Arg Ser Gln Thr Asp Thr Leu Glu Lys Val Gln Glu Arg Ala  
305 310 315 320

Asp Lys Phe Glu Ile Glu Asn Asn Thr Leu Lys Leu Lys Asn Ser Asp  
325 330 335

Leu Ser Phe Asn Asn Lys Ala Leu Lys Asp His Asn Asp Glu Leu Thr  
340 345 350

Glu Glu Leu Ser Asn Ala Lys Glu Lys Leu Arg Lys Asn Asp Lys Ser  
355 360 365

Leu Ser Glu Lys Ala Ser Lys Ile Gln Glu Leu Glu Ala Arg Lys  
370 375 380

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B1  
CMT